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1638

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/534,861A

DATE: 04/08/2002

TIME: 16:09:37

Input Set : A:\15313SEQ.txt  
 Output Set: N:\CRF3\04082002\I534861A.raw

3 <110> APPLICANT: Smeekens, J.C.M.  
 4 Ebskamp, Michael  
 5 Geerts, Hendrikis  
 6 Weisbeek, Petrus  
 8 <120> TITLE OF INVENTION: Production of Oligosaccharides in Transgenic Plants  
 10 <130> FILE REFERENCE: ARNO-1-15313  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/534,861A  
 13 <141> CURRENT FILING DATE: 2000-03-24  
 15 <150> PRIOR APPLICATION NUMBER: US 09/019,385  
 16 <151> PRIOR FILING DATE: 1998-02-05  
 18 <150> PRIOR APPLICATION NUMBER: US 09/193,385  
 19 <151> PRIOR FILING DATE: 1998-11-17  
 21 <150> PRIOR APPLICATION NUMBER: US 08/479,470  
 22 <151> PRIOR FILING DATE: 1995-06-07  
 24 <150> PRIOR APPLICATION NUMBER: NL 1000064  
 25 <151> PRIOR FILING DATE: 1995-04-05  
 27 <150> PRIOR APPLICATION NUMBER: NL 9401140  
 28 <151> PRIOR FILING DATE: 1994-08-07  
 30 <160> NUMBER OF SEQ ID NOS: 12  
 32 <170> SOFTWARE: PatentIn version 3.0  
 34 <210> SEQ ID NO: 1  
 35 <211> LENGTH: 2094  
 36 <212> TYPE: DNA  
 37 <213> ORGANISM: Barley  
 39 <220> FEATURE:  
 40 <221> NAME/KEY: CDS  
 41 <222> LOCATION: (46)..(1923)  
 43 <400> SEQUENCE: 1  
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 45 Met Gly Ser His  
 46 1  
 48 ggc aag cca ccg cta ccg tac gcc tac aag ccg ctg ccc tcg gac gcc 105  
 49 Gly Lys Pro Pro Leu Pro Tyr Ala Tyr Lys Pro Leu Pro Ser Asp Ala  
 50 5 10 15 20  
 52 gcc gac ggt aag ccg acc ggc tgc atg agg tgg tcc gcg tgt gcc acc 153  
 53 Ala Asp Gly Lys Arg Thr Gly Cys Met Arg Trp Ser Ala Cys Ala Thr  
 54 25 30 35  
 56 gtg ctg acg gcc tcg gcc atg gcg gtg gtg gtc ggc gcc acg ctc 201  
 57 Val Leu Thr Ala Ser Ala Met Ala Val Val Val Gly Ala Thr Leu  
 58 40 45 50  
 60 ctg gcg qga ttg aqg atg gag cag gcc gtc gac gag qag qcg qcg qcg 249  
 61 Leu Ala Gly Leu Arg Met Glu Gln Ala Val Asp Glu Glu Ala Ala Ala  
 62 55 60 65

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64	ggc	ggg	tcc	ccg	tgg	agc	aac	gag	atg	ctg	cag	tgg	cag	cgc	agc	ggt	297
65	Gly	Gly	Phe	Pro	Trp	Ser	Asn	Glu	Met	Leu	Gln	Trp	Gln	Arg	Ser	Gly	
66	70					75				80							
68	tac	cat	tcc	cag	acg	gcc	aag	aac	tac	atg	agc	gtt	ccc	aac	ggc	ctg	345
69	Tyr	His	Phe	Gln	Thr	Ala	Lys	Asn	Tyr	Met	Ser	Asp	Pro	Asn	Gly	Leu	
70	85					90				95						100	
72	atg	tat	tac	cgt	gga	tgg	tac	cac	atg	tcc	tac	cag	tac	aac	ccg	gtg	393
73	Met	Tyr	Tyr	Arg	Gly	Trp	Tyr	His	Met	Phe	Tyr	Gln	Tyr	Asn	Pro	Val	
74						105				110						115	
76	ggc	acc	gac	tgg	gac	gac	ggc	atg	gag	tgg	ggc	cac	gcc	gtg	tcc	ccg	441
77	Gly	Thr	Asp	Trp	Asp	Asp	Gly	Met	Glu	Trp	Gly	His	Ala	Val	Ser	Arg	
78						120				125						130	
80	aac	ctt	gtc	caa	tgg	ccg	acc	ctc	cct	atc	gcc	atg	gtg	gcc	gac	cag	489
81	Asn	Leu	Val	Gln	Trp	Arg	Thr	Leu	Pro	Ile	Ala	Met	Val	Ala	Asp	Gln	
82						135				140						145	
84	tgg	tac	gac	atc	ctc	gga	gtc	ctc	tgc	ggc	tcc	atg	acg	gtg	cta	ccc	537
85	Trp	Tyr	Asp	Ile	Leu	Gly	Val	Leu	Ser	Gly	Ser	Met	Thr	Val	Leu	Pro	
86						150				155						160	
88	aac	ggg	acg	gtc	atc	atg	atc	tac	acg	ggc	acc	aac	gcc	tcc	gcc		585
89	Asn	Gly	Thr	Val	Ile	Met	Ile	Tyr	Thr	Gly	Ala	Thr	Asn	Ala	Ser	Ala	
90	165					170				175						180	
92	gtg	gag	gtc	cag	tgc	atc	gcc	acc	ccg	gcc	gac	ccc	aac	gac	ccc	ctc	633
93	Val	Glu	Val	Gln	Cys	Ile	Ala	Thr	Pro	Ala	Asp	Pro	Asn	Asp	Pro	Leu	
94						185				190						195	
96	ctc	cgc	cg	tgg	acc	aag	cac	ccc	gcc	aac	ccc	gtc	atc	tgg	tgc	ccg	681
97	Leu	Arg	Arg	Trp	Thr	Lys	His	Pro	Ala	Asn	Pro	Val	Ile	Trp	Ser	Pro	
98						200				205						210	
100	ccg	ggg	gtc	ggc	acc	aag	gat	tcc	cga	gac	ccg	atg	acc	gcc	tgg	tac	729
101	Pro	Gly	Val	Gly	Thr	Lys	Asp	Phe	Arg	Asp	Pro	Met	Thr	Ala	Trp	Tyr	
102						215				220						225	
104	gac	gag	tcc	gac	gag	aca	tgg	ccg	acc	ctc	ctc	ggg	tcc	aag	gac	gac	777
105	Asp	Glu	Ser	Asp	Glu	Thr	Trp	Arg	Thr	Leu	Leu	Gly	Ser	Lys	Asp	Asp	
106						230				235						240	
108	cac	gac	ggc	cac	cac	gac	ggc	atc	qcc	atg	atg	tac	aag	acc	aag	gac	825
109	His	Asp	Gly	His	His	Asp	Gly	Ile	Ala	Met	Met	Tyr	Lys	Thr	Lys	Asp	
110	245					250				255						260	
112	tcc	ctc	aac	tac	gag	ctc	atc	ccg	ggc	atc	ttg	cac	ccg	gtg	gtg	ccg	873
113	Phe	Leu	Asn	Tyr	Glu	Leu	Ile	Pro	Gly	Ile	Leu	His	Arg	Val	Val	Arg	
114						265				270						275	
116	acc	ggc	gag	tgg	gag	tgc	atc	gac	ttc	tac	ccc	gtc	ggc	ccg	aga	agc	921
117	Thr	Gly	Glu	Trp	Glu	Cys	Ile	Asp	Phe	Tyr	Pro	Val	Gly	Arg	Arg	Ser	
118						280				285						290	
120	agc	qac	aac	tcg	tgc	gag	atg	ctg	cac	gtg	ttg	aag	gac	agc	atg	gac	969
121	Ser	Asp	Asn	Ser	Ser	Glu	Met	Leu	His	Val	Leu	Lys	Ala	Ser	Met	Asp	
122						295				300						305	
124	gac	qaa	ccg	cac	gac	tac	tac	tcg	ctg	ggc	acg	tac	gac	tcg	ccg	gcc	1017
125	Asp	Glu	Arg	His	Asp	Tyr	Tyr	Ser	Leu	Gly	Thr	Tyr	Asp	Ser	Ala	Ala	
126						310				315						320	
128	aac	acg	tgg	acg	ccc	atc	qac	ccg	qag	ctc	gac	ttg	ggg	atc	ggg	ctg	1065

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129 Asn Thr Trp Ile Pro Ile Asp Pro Glu Leu Asp Leu Gly Ile Gly Leu		
130 325 330 335 340		
132 aga tac gac tgg gga aag ttt tat gcg tcc acc tcc ttc tat gat ccg		1113
133 Arg Tyr Asp Trp Gly Lys Phe Tyr Ala Ser Thr Ser Phe Tyr Asp Pro		
134 345 350 355		
136 gcc aag aac cgg cgc qtg ctc atg ggg tac gtc ggc gag gtc gac tcc		1161
137 Ala Lys Asn Arg Arg Val Leu Met Gly Tyr Val Gly Glu Val Asp Ser		
138 360 365 370		
140 aag cgg gct gat gtc gtc aag gga tgg gct tcc att cag tca gtt cct		1209
141 Lys Arg Ala Asp Val Val Lys Gly Trp Ala Ser Ile Gln Ser Val Pro		
142 375 380 385		
144 agg acg gtg gct ctg gat gag aag acc cgg acg aac ctc ctg ctc tgg		1257
145 Arg Thr Val Ala Leu Asp Glu Lys Thr Arg Thr Asn Leu Leu Leu Trp		
146 390 395 400		
148 ccc gtt gag gag atc gag acc ctc cgc ctc aat gcc acg gaa ctg acc		1305
149 Pro Val Glu Glu Ile Glu Thr Leu Arg Leu Asn Ala Thr Glu Leu Thr		
150 405 410 415 420		
152 gac gtt acc att aac act ggc tcc gtc atc cat atc ccg ctc cgc caa		1353
153 Asp Val Thr Ile Asn Thr Gly Ser Val Ile His Ile Pro Leu Arg Gln		
154 425 430 435		
156 ggc act cac gct cga cat gcg gag gcc tct ttc cac ctt gat gct tcc		1401
157 Gly Thr His Ala Arg His Ala Glu Ala Ser Phe His Leu Asp Ala Ser		
158 440 445 450		
160 gcc gtg gct gcc ctc aac gag gcc gat gtg ggc tac aac tgc agt agc		1449
161 Ala Val Ala Ala Leu Asn Glu Ala Asp Val Gly Tyr Asn Cys Ser Ser		
162 455 460 465		
164 agc ggc ggc gct gtt aac cgc ggc gcg cta ggc ccc ttc ggc ctc ctc		1497
165 Ser Gly Gly Ala Val Asn Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu		
166 470 475 480		
168 gtc ctc gcc ggc ggt gac cgc cgt ggc gag caa acg gcg gtc tac ttc		1545
169 Val Leu Ala Ala Gly Asp Arg Arg Gly Glu Gln Thr Ala Val Tyr Phe		
170 485 490 495 500		
172 tac gtg tct agg ggc ctt gac gga ggc ctc cac acc acg ttc tgc caa		1593
173 Tyr Val Ser Arg Gly Leu Asp Gly Gly Leu His Thr Ser Phe Cys Gln		
174 505 510 515		
176 gat gag ctg aga tcg tca cga gcc aag gat gtg acc aag cgt gtc atc		1641
177 Asp Glu Leu Arg Ser Ser Arg Ala Lys Asp Val Thr Lys Arg Val Ile		
178 520 525 530		
180 ggg agc acg gtg ccg gtg ctc gac ggt gag gct ttg tca atg agg gtg		1689
181 Gly Ser Thr Val Pro Val Leu Asp Gly Glu Ala Leu Ser Met Arg Val		
182 535 540 545		
184 ctc gtg gat cac tcc atc gtg cag ggc ttc gac atg ggc ggg agg acc		1737
185 Leu Val Asp His Ser Ile Val Gln Gly Phe Asp Met Gly Gly Arg Thr		
186 550 555 560		
188 acg atg acc tcg ccg gtg tac ccg atg gag tcg tat cag gag gca aga		1785
189 Thr Met Thr Ser Arg Val Tyr Pro Met Glu Ser Tyr Gln Glu Ala Arg		
190 565 570 575 580		
192 gtc tac ttg ttc aac aac gcc acc ggt gcc acg gtg acg gcg gaa agg		1833
193 Val Tyr Leu Phe Asn Asn Ala Thr Gly Ala Ser Val Thr Ala Glu Arg		

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196	ctg gtc gtg cac gag atg gac tcg gca cac aac cag ctc tcc aat gag			1881
197	Leu Val Val His Glu Met Asp Ser Ala His Asn Gln Leu Ser Asn Glu			
198	600	605	610	
200	gac gat ggc atg tat ctt cat caa gtt ctt gaa tct cgt cat			1923
201	Asp Asp Gly Met Tyr Leu His Gln Val Leu Glu Ser Arg His			
202	615	620	625	
204	taataagcta cattggatca aagaagatca ccagggagg gcaattcata cataaatcga			1983
206	atcattctgc acaacctcgc ttgcagcatg cattgaaaca tctgttattt gatcatctc			2043
208	tccatattatg tcatagtcaa ctatattact ttgtaaaaaa aaaaaaaaaa a			2094
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212	<211> LENGTH: 626			
213	<212> TYPE: PRT			
214	<213> ORGANISM: Barley			
216	<400> SEQUENCE: 2			
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223	20 25 30			
226	Ala Cys Ala Thr Val Leu Thr Ala Ser Ala Met Ala Val Val Val			
227	35 40 45			
230	Gly Ala Thr Leu Leu Ala Gly Leu Arg Met Glu Gln Ala Val Asp Glu			
231	50 55 60			
234	Glu Ala Ala Ala Gly Gly Phe Pro Trp Ser Asn Glu Met Leu Gln Trp			
235	65 70 75 80			
238	Gln Arg Ser Gly Tyr His Phe Gln Thr Ala Lys Asn Tyr Met Ser Asp			
239	85 90 95			
242	Pro Asn Gly Leu Met Tyr Tyr Arg Gly Trp Tyr His Met Phe Tyr Gln			
243	100 105 110			
246	Tyr Asn Pro Val Gly Thr Asp Trp Asp Asp Gly Met Glu Trp Gly His			
247	115 120 125			
250	Ala Val Ser Arg Asn Leu Val Gln Trp Arg Thr Leu Pro Ile Ala Met			
251	130 135 140			
254	Val Ala Asp Gln Trp Tyr Asp Ile Leu Gly Val Leu Ser Gly Ser Met			
255	145 150 155 160			
258	Thr Val Leu Pro Asn Gly Thr Val Ile Met Ile Tyr Thr Gly Ala Thr			
259	165 170 175			
262	Asn Ala Ser Ala Val Glu Val Gln Cys Ile Ala Thr Pro Ala Asp Pro			
263	180 185 190			
266	Asn Asp Pro Leu Leu Arg Arg Trp Thr Lys His Pro Ala Asn Pro Val			
267	195 200 205			
270	Ile Trp Ser Pro Pro Gly Val Gly Thr Lys Asp Phe Arg Asp Pro Met			
271	210 215 220			
274	Thr Ala Trp Tyr Asp Glu Ser Asp Glu Thr Trp Arg Thr Leu Leu Gly			
275	225 230 235 240			
278	Ser Lys Asp Asp His Asp Gly His His Asp Gly Ile Ala Met Met Tyr			
279	245 250 255			
282	Lys Thr Lys Asp Phe Leu Asn Tyr Glu Leu Ile Pro Gly Ile Leu His			
283	260 265 270			

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286 Arg Val Val Arg Thr Gly Glu Trp Glu Cys Ile Asp Phe Tyr Pro Val  
 287 275 280 285  
 290 Gly Arg Arg Ser Ser Asp Asn Ser Ser Glu Met Leu His Val Leu Lys  
 291 290 295 300  
 294 Ala Ser Met Asp Asp Glu Arg His Asp Tyr Tyr Ser Leu Gly Thr Tyr  
 295 305 310 315 320  
 298 Asp Ser Ala Ala Asn Thr Trp Thr Pro Ile Asp Pro Glu Leu Asp Leu  
 299 325 330 335  
 302 Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Phe Tyr Ala Ser Thr Ser  
 303 340 345 350  
 306 Phe Tyr Asp Pro Ala Lys Asn Arg Arg Val Leu Met Gly Tyr Val Gly  
 307 355 360 365  
 310 Glu Val Asp Ser Lys Arg Ala Asp Val Val Lys Gly Trp Ala Ser Ile  
 311 370 375 380  
 314 Gln Ser Val Pro Arg Thr Val Ala Leu Asp Glu Lys Thr Arg Thr Asn  
 315 385 390 395 400  
 318 Leu Leu Leu Trp Pro Val Glu Glu Ile Glu Thr Leu Arg Leu Asn Ala  
 319 405 410 415  
 322 Thr Glu Leu Thr Asp Val Thr Ile Asn Thr Gly Ser Val Ile His Ile  
 323 420 425 430  
 326 Pro Leu Arg Gln Gly Thr His Ala Arg His Ala Glu Ala Ser Phe His  
 327 435 440 445  
 330 Leu Asp Ala Ser Ala Val Ala Ala Leu Asn Glu Ala Asp Val Gly Tyr  
 331 450 455 460  
 334 Asn Cys Ser Ser Ser Gly Gly Ala Val Asn Arg Gly Ala Leu Gly Pro  
 335 465 470 475 480  
 338 Phe Gly Leu Leu Val Leu Ala Ala Gly Asp Arg Arg Gly Glu Gln Thr  
 339 485 490 495  
 342 Ala Val Tyr Phe Tyr Val Ser Arg Gly Leu Asp Gly Gly Leu His Thr  
 343 500 505 510  
 346 Ser Phe Cys Gln Asp Glu Leu Arg Ser Ser Arg Ala Lys Asp Val Thr  
 347 515 520 525  
 350 Lys Arg Val Ile Gly Ser Thr Val Pro Val Leu Asp Gly Glu Ala Leu  
 351 530 535 540  
 354 Ser Met Arg Val Leu Val Asp His Ser Ile Val Gln Gly Phe Asp Met  
 355 545 550 555 560  
 358 Gly Gly Arg Thr Thr Met Thr Ser Arg Val Tyr Pro Met Glu Ser Tyr  
 359 565 570 575  
 362 Gln Glu Ala Arg Val Tyr Leu Phe Asn Asn Ala Thr Gly Ala Ser Val  
 363 580 585 590  
 366 Thr Ala Glu Arg Leu Val Val His Glu Met Asp Ser Ala His Asn Gln  
 367 595 600 605  
 370 Leu Ser Asn Glu Asp Asp Gly Met Tyr Leu His Gln Val Leu Glu Ser  
 371 610 615 620  
 374 Arg His  
 375 625  
 378 <210> SEQ ID NO: 3  
 379 <211> LENGTH: 30  
 380 <212> TYPE: DNA

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:474 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12